

In the Abstract:

Please amend the abstract as follows:

-- The present invention relates to a A method for the detection of the methylation status of a nucleotide at a predetermined position in a nucleic acid molecule is disclosed. The method involves comprising the steps of (a) treating a sample comprising said the nucleic acid molecule or consisting of said nucleic acid molecule in an aqueous solution with an agent suitable for the conversion of said the nucleotide if present in (i) methylated form; or (ii) non-methylated form, to pair with a nucleotide normally not pairing with said the nucleotide prior to conversion; (b) amplifying said the nucleic acid molecule treated with said the agent; (c) real-time sequencing said the amplified nucleic acid molecule; and (d) detecting whether said the nucleotide is asformerly methylated or not methylated in said the predetermined position in the sample. The invention further relates to Also disclosed is a method for the diagnosis of a pathological condition or the predisposition for a pathological condition comprising detection of a methylation status of a nucleotide at a predetermined position in a nucleic acid molecule comprising the steps of (a) treating a sample comprising said nucleic acid molecule or consisting of said nucleic acid molecule in an aqueous solution with an agent suitable for the conversion of said nucleotide if present in (i) methylated form; or (ii) non-methylated form to pair with a nucleotide normally not pairing with said nucleotide prior to conversion; (b) amplifying said nucleic acid molecule treated with said agent; (c) real-time sequencing said amplified nucleic acid molecule; and (d) detecting whether said nucleotide is formerly methylated or not methylated in said the predetermined position in the sample wherein Here, a methylated or not non-methylated nucleotide is indicative of a the pathological condition or the predisposition for said the pathological condition. --